

cells with PE-labeled goat anti-human Ig to detect chimeric SDF-Fc polypeptide remaining after the 3- or 15-hour incubation (data not shown).

Down-regulation of receptor by binding of MIP-1 α -Fc and MIP-1 β -Fc chimeric polypeptides to cells is determined by an assay for receptor down-regulation analogous to that described above.

5
SEQUENCE LISTING

10 (1) GENERAL INFORMATION:

(i) APPLICANT: Herrmann, Steve
Swanberg, Stephen

15 (ii) TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
CHEMOKINE DOMAINS

(iii) NUMBER OF SEQUENCES: 10

20 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark
(C) CITY: Cambridge
(D) STATE: MA
25 (E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
35 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne
40 (B) REGISTRATION NUMBER: P-41,323
(C) REFERENCE/DOCKET NUMBER: GI5291

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8284
45 (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Ala Lys Val Val Val Val Leu Val Val Leu Val Leu Thr Ala Leu
 1 5 10 15

Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
 20 25 30

Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
 35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
 50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
 65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys Gly Ser Gly Ser Gly Ser Gly
 85 90 95

Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala
 100 105 110

Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 115 120 125

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 130 135 140

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 145 150 155 160

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 165 170 175

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 180 185 190

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 195 200 205

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 210 215 220

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
 225 230 235 240

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 245 250 255

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 260 265 270

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACA CAGAAGAGCC TCTCCCTGTC 1200
 TCTGGGTAAA TGATAAGAAT TC 1222

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20 Met Asn Ala Lys Val Val Val Val Leu Val Val Leu Val Thr Ala Leu
 1 5 10 15
 Cys Leu Ser Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe
 20 25 30
 25 Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu
 35 40 45
 30 Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn
 50 55 60
 Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr
 65 70 75 80
 35 Leu Glu Lys Ala Leu Asn Lys Gly Ser Gly Ser Gly Ser Gly
 85 90 95
 Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu
 100 105 110
 40 Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 115 120 125
 45 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 130 135 140
 Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 145 150 155 160
 50 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 165 170 175
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 180 185 190
 55 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 195 200 205
 60 Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 210 215 220
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
 225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 245 250 255
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 5 260 265 270
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
 275 280 285
 Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
 10 290 295 300
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 305 310 315 320
 15 Ser Leu Ser Leu Gly Lys
 325

20 (2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear
 (iii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35	GCAGGCCGCGC CATGAACGCC AAGGTCGTGG TCGTGCTGGT CCTCGTGCTG ACCGCGCTCT	60
	GCCTCAGCAA GCCCGTCAGC CTGAGCTACA GATGCCCATG CCGATTCTTC GAAAGCCATG	120
	TTGCCAGAGC CAACGTCAAG CATCTAAAA TTCTAACAC TCCAAACTGT GCCCTTCAGA	180
40	TTGTAGCCCG GCTGAAGAAC AACAACAGAC AAGTGTGCAT TGACCCGAAG CTAAAGTGGA	240
	TTCAGGAGTA CCTGGAGAAA GCTTTAAACA AGGGATCCGG CTCTGGGAGC GGCTCTGGCT	300
	CTGAGTCAA ATATGGTCCC CCATGCCAT CATGTCCAGG TAAGCCAACC CAGGCCTCGC	360
45	CCTCCAGCTC AAGGCGGGAC AGGTGCCCTA GAGTAGCCTG CATCCAGGGC CAGGCCAG	420
	CCGGGTGCTG ACGCATCCAC CTCCATCTCT TCCTCAGCAC CTGAGTTCGA GGGGGCACCA	480
50	TCAGTCTTCC TGTCCCCCCC AAAACCCAAG GACACTCTCA TGATCTCCCG GACCCCTGAG	540
	GTCACGTGCG TGGTGGTGGA CGTGAGCCAG GAAGACCCCG AGGTCCAGTT CAACTGGTAC	600
	GTGGATGGCG TGGAGGTGCA TAATGCCAAG ACAAAAGCCGC GGGAGGAGCA GTTCAACAGC	660
55	ACGTACCGTG TGGTCAGCGT CCTCACCGTC CTGCACCGAG ACTGGCTGAA CGGCAAGGAG	720
	TACAAGTGCA AGGTCTCCAA CAAAGGCCCTC CCGTCCTCCA TCGAGAAAAC CATCTCCAAA	780
60	GCCAAAGGTG GGACCCACGG GGTGCGAGGG CCACACGGAC AGAGGTCAAGC TCGGCCACC	840
	CTCTGCCCTG GGAGTGACCG CTGTGCCAAC CTCTGTCCCT ACAGGGCAGC CCCGAGAGCC	900

	ACAGGGTGTAC ACCCTGCCCC CATCCCAGGA GGAGATGACC AAGAACCAAGG TCAGCCTGAC	960
	CTGCCTGGTC AAAGGCTTCT ACCCCAGCGA CATGCCGTG GAGTGGGAGA GCAATGGGCA	1020
5	GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT	1080
	CTACAGCAGG CTAACCGTGG ACAAGAGCAG GTGGCAGGAG GGGAAATGTCT TCTCATGCTC	1140
10	CGTGATGCAT GAGGCTCTGC ACAACCACTA CACACAGAAG AGCCTCTCCC TGTCTCTGGG	1200
	TAAATGATAA GAATTC	1216

(2) INFORMATION FOR SEQ ID NO:5:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 331 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS:
	(D) TOPOLOGY: linear
20	(ii) MOLECULE TYPE: protein

25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
	Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
	1 5 10 15
30	Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
	20 25 30
35	Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
	35 40 45
	Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
	50 55 60
40	Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
	65 70 75 80
	Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala Gly Ser Gly Ser'
	85 90 95
45	Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
	100 105 110
	Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro
50	115 120 125
	Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
	130 135 140
55	Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
	145 150 155 160
	Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
60	165 170 175
	Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
	180 185 190

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 195 200 205
 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 5 210 215 220
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 225 230 235 240
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 10 245 250 255
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 260 265 270
 15 Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 275 280 285
 Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 20 290 295 300
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 305 310 315 320
 25 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: cDNA

 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 GCGGCCGCC AATCATGCAG GTCTCCACTG CTGCCCTTGC TGTCCCTCCTC TGCACCATGG 60
 45 CTCTCTGCAA CCAGTTCTCT GCATCACTTG CTGCTGACAC GCCGACCGGCC TGCTGCTTCA 120
 GCTACACCTC CCGGCAGATT CCACAGAATT TCATAGCTGA CTACTTGAG ACGAGCAGCC 180
 50 AGTGCTCCAA GCCCGGTGTC ATCTTCCTAA CCAAGCGAAG CCGGCAGGTC TGTGCTGACC 240
 CCAAGTGAGGA GTGGGTCCAG AAATACGTCA GTGACCTGGA GCTGAGTGCC GGATCCGGCT 300
 CTGGGAGCGG CTCTGGCTCT GAGTCCAAAT ATGGTCCCCC ATGCCCATCA TGTCCAGGTA 360
 55 AGCCAACCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA GTAGCCTGCA 420
 TCCAGGGACA GGCCCCAGCC GGGTGCTGAC GCATCCACCT CCATCTCTTC CTCAGCACCT 480
 60 GAGTTCGAGG GGGCACCATC AGTCTTCCTG TTCCCCCAA AACCCAAGGA CACTCTCATG 540
 ATCTCCCGGA CCCCTGAGGT CACGTGCGTG GTGGTGGACG TGAGCCAGGA AGACCCCGAG 600
 GTCCAGTTCA ACTGGTACGT GGATGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCCGGG 660

	GAGGAGCAGT TCAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCCT GCACCAGGAC	720
	TGGCTGAACG GCAAGGAGTA CAAAGTGAAG GTCTCCAACA AAGGCCTCCC GTCCTCCATC	780
5	GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCACGGGG TGCGAGGGCC ACACGGACAG	840
	AGGTCACTCTC GGCCCACCCCT CTGCCCTGGG AGTGACCGCT GTGCCAACCT CTGTCCTAC	900
10	AGGGCAGCCC CGAGAGCCAC AGGTGTACAC CCTGCCCTCA TCCCAGGAGG AGATGACCAA	960
	GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA	1020
	GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC	1080
15	CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT GGCAGGAGGG	1140
	GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA CACAGAAGAG	1200
	CCTCTCCCTG TCTCTGGTA AATGATAAGA ATT	1234
20	(2) INFORMATION FOR SEQ ID NO:7:	

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 331 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS:	
	(D) TOPOLOGY: linear	

30	(ii) MOLECULE TYPE: protein	
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35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
	Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala	
	1 5 10 15	
40	Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr	
	20 25 30	
	Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val	
	35 40 45	
45	Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val	
	50 55 60	
	Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser	
50	65 70 75 80	
	Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn Gly Ser Gly Ser	
	85 90 95	
55	Gly Ser Gly Ser Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser	
	100 105 110	
	Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro	
	115 120 125	
60	Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr	
	130 135 140	
	Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn	

	145	150	155	160
	Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg			
	165 170 175			
5	Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val			
	180 185 190			
10	Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser			
	195 200 205			
	Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys			
	210 215 220			
15	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu			
	225 230 235 240			
	Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe			
20	245 250 255			
	Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu			
	260 265 270			
25	Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe			
	275 280 285			
	Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly			
	290 295 300			
30	Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr			
	305 310 315 320			
	Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys			
	325 330			

35 (2) INFORMATION FOR SEQ ID NO:8:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50	GC GGCCGCCA ATACCATGAA GCTCTGCGTG ACTGTCTGTG CTCTCCTCAT GCTAGTAGCT	60
	GCCTTCTGCT CTCCAGCGCT CTCAGCACCA ATGGGCTCAG ACCCTCCCAC CGCCTGCTGC	120
55	TTTTCTTACA CCGCGAGGAA GCTTCCTCGC AACTTTGTGG TAGATTACTA TGAGACCAGC	180
	AGCCTCTGCT CCCAGCCAGC TGTGGTATTG CAAACCAAAA GAAGCAAGCA AGTCTGTGCT	240
60	GATCCCAGTG AATCCTGGGT CCAGGAGTAC GTGTATGACC TGGAACTGAA CGGATCCGGC	300
	TCTGGGAGCG GCTCTGGCTC TGAGTCCAAA TATGGTCCCC CATTGCCATC ATGTCCAGGT	360
	AAGCCAACCC AGGCCTCGCC CTCCAGCTCA AGGCGGGACA GGTGCCCTAG AGTAGCCCTGC	420

	ATCCAGGGAC AGGCCCCAGC CGGGTGCTGA CGCATCCACC TCCATCTCTT CCTCAGCACC	480
	TGAGTTCGAG GGGGCACCAT CAGTCCTCCT GTTCCCCCA AAACCCAAGG AACTCTCAT	540
5	GATCTCCCGG ACCCCTGAGG TCACGTGCGT GGTGGTGGAC GTGAGCCAGG AAGACCCCGA	600
	GGTCCAGTTC AACTGGTACG TGGATGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG	660
10	GGAGGAGCAG TTCAACAGCA CGTACCGTGT GGTCAGCGTC CTCACCGTCC TGCACCAGGA	720
	CTGGCTGAAC GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC AAAGGCCTCC CGTCCTCCAT	780
	CGAGAAAACC ATCTCCAAAG CCAAAGGTGG GACCCACGGG GTGCGAGGGC CACACGGACA	840
15	GAGGTCAGCT CGGCCCCACCC TCTGCCCTGG GAGTGACCGC TGTGCCAAC TCTGTCCCTA	900
	CAGGGCAGCC CCGAGAGCCA CAGGTGTACA CCCTGCCCTT ATCCCAGGAG GAGATGACCA	960
20	AGAACCCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC ATCGCCGTGG	1020
	AGTGGGAGAG CAATGGGCAG CCGGAGAACAA ACTACAAGAC CACGCCTCCCC GTGCTGGACT	1080
	CCGACGGCTC CTTCCTCCTC TACAGCAGGC TAACCGTGGCA CAAGAGCAGG TGGCAGGAGG	1140
25	GGAATGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC ACACAGAAGA	1200
	GCCTCTCCCT GTCTCTGGGT AAATGATAAG AATTC	1235

(2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 45 Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
 1 5 10 15
 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
 20 25 30
 50 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
 35 40 45
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
 55 50 55 60
 55 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
 65 70 75 80
 60 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15	Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala	1	5	10	15
	Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr	20	25	30	
20	Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val	35	40	45	
	Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val	50	55	60	
25	Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser	65	70	75	80
30	Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn	85	90		